100% hits SID 4 GenBank & GeneSeq & Patents

```
LOCUS       HVDNAHOR3               1859 bp    DNA     linear   PLN 25-APR-1996
DEFINITION  H.vulgare Hor3 gene.
ACCESSION   X84368
VERSION     X84368.1  GI:671536
KEYWORDS    D hordein; Hor3 gene.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 1859)
  AUTHORS   Sorensen,M.B., Muller,M., Skerritt,J. and Simpson,D.
  TITLE     Hordein promoter methylation and transcriptional activity in
            wild-type and mutant barley endosperm
  JOURNAL   Mol. Gen. Genet. 250 (6), 750-760 (1996)
  MEDLINE   96204516
REFERENCE   2  (bases 1 to 1859)
  AUTHORS   Sorensen,M.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-FEB-1995) M.B. Sorensen, Carlsberg Laboratory,
            Department of Physiology, Gamle Carlsbergvej 1, DK-2500 Valby,
            DENMARK
COMMENT     Sequence overlapping with that under the accession number X68072.
FEATURES             Location/Qualifiers
     source          1. .1859
                     /organism="Hordeum vulgare"
                     /variety="Bomi"
                     /db_xref="taxon:4513"
                     /chromosome="5"
                     /map="1H long arm"
                     /clone="pHor3-1"
                     /tissue_type="endosperm"
                     /clone_lib="lambda Zap II"
                     /dev_stage="seed"
     TATA_signal     343. .349
     gene            435. .1859
                     /gene="Hor3"
     CDS             435. .>1859
                     /gene="Hor3"
                     /codon_start=1
                     /product="D-hordein"
                     /protein_id="CAA59104.1"
                     /db_xref="GI:671537"
                     /db_xref="SPTREMBL:Q40045"
                     /translation="MAKRLVLFVAVIVALVALTTAEREINGNNIFLDSRSRQLQCERE
                     LQESSLEACRRVVDQQLVGQLPWSTGLQMQCCQQLRDVSPECRPVALSQVVRQYEQQT
                     EVPSKGGSFYPGGTAPPLQQGGWWGTSVKWNYPDQTSSQQSWQGQQGYHQSVTSSQQP
                     GQGQQGSYPGSTFPQQPGQGQQPGQRQPWSYPSATFPQQPGQGQGQQGYYPGATSLLQ
                     PGQGQQGPYQSATSPQQPGQGQGQQETYPIATSPHQPGQWQQPGQGQQGYYPSVTSPQ
                     QSGQGQQGYPSTTSPQQSGQGQQLGQGQQPGQGQQGYPSATFPQQPGQWQQGSYPSTT
                     SPQQSGQGQQGYNPSGTSTQQSGQVHQLGQGQQGYYPIATSPQQPGQGQQLGQGQQPG
                     HGQQLVQGQQQGQGQQGHYPSMTSPHQTGQGQKGYYPSAISPQQSGQGQQGYQPSGAS
                     SQGSVQGACQHSTSSPQQQAQGCQA"
     mat_peptide     498. .>1859
                     /gene="Hor3"
                     /product="unnamed"
     variation       1500
```

```
                     /gene="Hor3"
     variation       1514
                     /gene="Hor3"
     variation       1810
                     /gene="Hor3"
BASE COUNT      548 a    550 c    462 g    299 t
ORIGIN


alignment_scores:
            Quality:   86.00              Length:      20
              Ratio:  4.300                Gaps:       0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-538-864-4 x HVDNAHOR3    ..

 Align seg 1/1  to: HVDNAHOR3  from: 1  to: 1859

       1 AlaLysArgLeuValLeuPheValAlaValIleValAlaLeuValAlaLe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     438 GCTAAGCGGCTGGTCCTCTTTGTGGCGGTAATCGTCGCCCTCGTGGCTCT 487

      17 uThrThrAla 20
         ||||||||||
     488 CACCACCGCT 497

seq_name: gb_pl:BLYHOR3
```

```
seq_documentation_block:
LOCUS       BLYHOR3                 2296 bp    mRNA    linear   PLN 06-FEB-1999
DEFINITION  Barley Hor3 mRNA for D hordein, complete cds.
ACCESSION   D82941
VERSION     D82941.1  GI:1167497
KEYWORDS    D hordein; Hor3.
SOURCE      Hordeum vulgare (strain:Haruna Nijo) Seed Endosperm cDNA to mRNA,
            clone:DH4.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 2296)
  AUTHORS   Hirota,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-1996) Naohiko Hirota, Plant Bioengineering
            Research Laboratories,Sapporo breweries, Biotechnology department;
            Kizaki 37-1, Nitta, Gunma 370-03, Japan
            (E-mail:sapplant@po.infosphere.or.jp, Tel:0276-56-1455,
            Fax:0276-56-1605)
REFERENCE   2  (bases 1 to 2296)
  AUTHORS   Hirota,N., Kuroda,H. and Ito,K.
  JOURNAL   Unpublished (1996)
FEATURES             Location/Qualifiers
     source          1. .2296
                     /organism="Hordeum vulgare"
                     /strain="Haruna Nijo"
                     /db_xref="taxon:4513"
                     /clone="DH4"
                     /tissue_type="Endosperm"
                     /dev_stage="Seed"
     gene            37. .2160
                     /gene="Hor3"
     sig_peptide     37. .120
                     /gene="Hor3"
     CDS             37. .2160
                     /gene="Hor3"
                     /function="seed storage"
                     /codon_start=1
                     /product="D hordein"
                     /protein_id="BAA11642.1"
                     /db_xref="GI:1167498"
                     /translation="MAKRLVLFVAVIVALVALTTAEREINGNNIFLDSRSRQLQCERE
                     LQESSLEACRRVVDQQLVGQLPWSTGLQMQCCQQLRDVSPECRPVALSQVVRQYEQQT
                     EVPSKGGSFYPGGTAPPLQQGGWWGTSVKWYYPDQTSSQQSWQGQQGYHQSVTSSQQP
                     GQGQQGSYPGSTFPQQPGQGQQPGQRQPWSYPSATFPQQPGQGQGQQGYYPGATSLLQ
                     PGQGQQGPYQSATSPQQPGQGQGQQETYPIATSPHQPGQWQQPGQGQQGFYPSVTSPQ
                     QSGQGQQGYPSTTSPQQSGQGQQLGQGQQPGQGQQGYPSATFPQQPGQWQQGSYPSTT
                     SPQQSGQGQQGYNPSGTSTQQPGQVQQLGQGQQGYYPIATSPQQPGQGQQLGQGQQPG
                     HGQQLVQGQQQGQGQQGHYPSMTSPHQTGQGQKGYYPSAISPQQSGQGQQGYQPSGAS
                     SQGSVQGACQHSTSSPQQQAQGCQASSPKQGLGSLYYPSGAYTQQKPGQGYNPGGTSP
                     LHQQGGGFGGGLTTEQPQGGKQPFHCQQTTVSPHQGQQTTVSPHQGQQTTVSPHQGQQ
                     TTVSPHQGQQTTVSPHQGQQTTVSPHQGQQTTVSPHPGQQTTVSPHQGQQTTVSPHQG
                     QQTTVSPHQGQQPGEQPCGFPGQQTTVSLHHGQQSNELYYGSPYHVSVEQPSASLKVA
                     KAQQLAAQLPAMCRLEGGGGLLASQ"
     mat_peptide     121. .2157
                     /gene="Hor3"
```

```
                    /product="D hordein"
     polyA_signal    2214. .2219
     polyA_signal    2267. .2272
BASE COUNT      629 a    708 c    606 g    353 t
ORIGIN


alignment_scores:
            Quality:   86.00              Length:     20
              Ratio:  4.300                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-538-864-4 x BLYHOR3    ..

 Align seg 1/1  to: BLYHOR3  from: 1  to: 2296

       1 AlaLysArgLeuValLeuPheValAlaValIleValAlaLeuValAlaLe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      40 GCTAAGCGGCTGGTCCTCTTTGTGGCGGTAATCGTCGCCCTCGTGGCTCT 89

      17 uThrThrAla 20
         ||||||||||
      90 CACCACCGCT 99

seq_name: gb_pat:BD005223

seq_documentation_block:
LOCUS        BD005223               2380 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION   Method of production of barley reduced gel protein.
ACCESSION    BD005223
VERSION      BD005223.1  GI:18633184
KEYWORDS     JP 03075311-T/2.
SOURCE       unidentified.
  ORGANISM   unidentified
             unclassified.
REFERENCE    1  (bases 1 to 2380)
  AUTHORS    Hirota,N., Kihara,M. and Ito,K.
  TITLE      Method of production of barley reduced gel protein
  JOURNAL    Patent: JP 03075311-T 2 16-FEB-2001;
             SAPPORO BREWERIES LTD,NAOHIKO HIROTA,MAKOTO KIHARA,KAZUTOSHI ITO
COMMENT      OS   Hordenum vulgare (barley)
             PN   JP 03075311-T/2
             PD   16-FEB-2001
             PF   16-AUG-2000 JP 2000005476
             PR   16-AUG-1999 JP 99P   229696
             PI   NAOHIKO HIROTA,MAKOTO KIHARA,KAZUTOSHI ITO
             PC   A01H5/00,C12N15/10,C12N15/63
             CC
             FH   Key             Location/Qualifiers
             FT   source          1. .2380
             FT                   /organism='Hordenum vulgare (barley)'.
FEATURES             Location/Qualifiers
     source          1. .2380
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      642 a    747 c    622 g    369 t
```

ORIGIN

alignment_scores:
Quality: 86.00 Length: 20
Ratio: 4.300 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-538-864-4 x BD005223 ..

Align seg 1/1 to: BD005223 from: 1 to: 2380

```
      1 AlaLysArgLeuValLeuPheValAlaValIleValAlaLeuValAlaLe 17
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     27 GCTAAGCGGCTGGTCCTCTTTGTGGCGGTAATCGTCGCCCTCGTGGCTCT 76

     17 uThrThrAla 20
        |||||||||
     77 CACCACCGCT 86
```

seq_documentation_block:
ID AAX34625 standard; DNA; 497 BP.
XX
AC AAX34625;
XX
DT 01-JUL-1999 (first entry)
XX
DE Barley D hordein promoter and signal sequence.
XX
KW Seed maturation-specific promoter; seed; transgenic plant; rice; barley;
KW maize; wheat; oat; rye; sorghum; millet; tricalate plant; insulin;
KW interferon; erythropoietin; interleukin; nutritional supplement;
KW grain quality; D hordein promoter; signal sequence; ss.
XX
OS Hordeum vulgare.
XX
FH Key   Location/Qualifiers
FT CDS   434..497
FT   /*tag= a
FT   /note= "fragment encoding barley D hordein
FT   signal peptide"
XX
PN WO9916890-A2.
XX
PD 08-APR-1999.
XX
PF 30-SEP-1998;   98WO-US20691.
XX
PR 30-SEP-1997;   97US-0060510.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Buchanan RB, Cho M, Lemaux PG;
XX
DR WPI; 1999-255099/21.
DR P-PSDB; AAY06898.
XX
PT New recombinant nucleic acid molecules
XX
PS Examples; Fig 5; 48pp; English.
XX
CC The invention relates to recombinant nucleic acid molecules which contain
CC a seed maturation-specific promoter for expression of a selected
CC polypeptide in seeds of transgenic plants. The novel recombinant nucleic
CC acid molecule (NAM) has a structure P-X or P-SS-X, where X is a NAM
CC encoding a polypeptide, P is a seed maturation-specific promoter, and SS
CC is a signal sequence that targets a linked polypeptide to an
CC intracellular body. The recombinant NAMs can be used for producing
CC transgenic plants such as rice, barley, maize, wheat, oat, rye, sorghum,
CC millet or tricalate plants. The transgenic plants can be used for
CC producing a selected polypeptide in seeds of the plants. They can be
CC used to produce polypeptides such as insulin, interferons, erythropoietin
CC and interleukins, or nutritional supplements. Alternatively the
CC polypeptide can improve the quality of grain. The present sequence
CC represents the nucleic acid sequence of a barley D hordein promoter and
CC signal sequence.

```
XX
SQ   Sequence 497 BP; 138 A; 150 C; 89 G; 120 T; 0 other;


alignment_scores:
            Quality:   86.00              Length:     20
              Ratio:  4.300                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-538-864-4 x AAX34625   ..

 Align seg 1/1  to: AAX34625  from: 1  to: 497

       1 AlaLysArgLeuValLeuPheValAlaValIleValAlaLeuValAlaLe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     438 GCTAAGCGGCTGGTCCTCTTTGTGGCGGTAATCGTCGCCCTCGTGGCTCT 487

      17 uThrThrAla 20
         ||||||||||
     488 CACCACCGCT 497

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAC61536

seq_documentation_block:
ID   AAC61536 standard; DNA; 497 BP.
XX
AC   AAC61536;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Nucleotide sequence of the D-hordein promoter and signal sequence.
XX
KW   Transgenic plant; thioredoxin; edible seed; food; feed; beverage;
KW   allergenicity; germination rate; flour; malabsorption syndrome;
KW   coeliac disease; sprue; catarrhal dysentery; brewing; malting;
KW   industrial alcohol; food additive; D-hordein promoter; ss.
XX
OS   Hordeum vulgare.
XX
FH   Key             Location/Qualifiers
FT   promoter        1..434
FT                   /*tag=  a
FT   sig_peptide     435..497
FT                   /*tag=  b
XX
PN   WO200058453-A2.
XX
PD   05-OCT-2000.
XX
PF   29-MAR-2000; 2000WO-US08315.
XX
PR   29-MAR-1999;   99US-0126736.
PR   31-MAR-1999;   99US-0127198.
PR   06-DEC-1999;   99US-0169162.
PR   21-JAN-2000; 2000US-0177739.
PR   21-JAN-2000; 2000US-0177740.
```

XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Cho M, Lemaux PG, Buchanan BB, Wong J, Marx C;
XX
DR WPI; 2000-611708/58.
XX
PT Transgenic plants overexpressing thioredoxin protein, and their
PT applications to enhance baking quality, digestibility, brewing and
PT malting operations, and reduce allergenicity -
XX
PS Example 1; Fig 7; 103pp; English.
XX
CC The specification describes transgenic plants in which have an increased
CC specific activity of thioredoxin compared to a non-transgenic plant of
CC the same species. The transgenic plants provide edible seeds or grains
CC for processing and consumption as food, feed, or beverage products by
CC humans and other animals which have reduced allergenicity, increased
CC digestibility, and improved germination rate. For humans, particular
CC food products improved which can be improved include flour, as bread,
CC pasta, cookies, and cake. The dough has increased strength and volume,
CC improving baking qualities. Improved enzyme contents (pullulanase and
CC amylase) improve digestibility of endogenous starches and proteins,
CC reducing malabsorption syndromes in certain subjects (e.g., coeliac
CC disease, sprue, and catarrhal dysentery patients), and allowing wider
CC consumption. Fermentability, of application in the brewing and malting
CC industries, and for production of industrial alcohol and malt as such,
CC is also improved. Products from transgenic plants may also be used as
CC food additives. The present sequence represents the barley
CC endosperm-specific D-hordein promoter and the signal sequence. It is
CC used in the course of the invention, to produce transgenic plants.
XX
SQ Sequence 497 BP; 138 A; 150 C; 89 G; 120 T; 0 other;

alignment_scores:
Quality: 86.00 Length: 20
Ratio: 4.300 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-538-864-4 x AAC61536 ..

Align seg 1/1 to: AAC61536 from: 1 to: 497

```
      1 AlaLysArgLeuValLeuPheValAlaValIleValAlaLeuValAlaLe 17
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    438 GCTAAGCGGCTGGTCCTCTTTGTGGCGGTAATCGTCGCCCTCGTGGCTCT 487

     17 uThrThrAla 20
        |||||||||
    488 CACCACCGCT 497
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAC62462

seq_documentation_block:
ID AAC62462 standard; cDNA; 497 BP.

XX
AC AAC62462;
XX
DT 07-FEB-2001 (first entry)
XX
DE Barley D-hordein promoter and signal sequence.
XX
KW Barley; thioredoxin h; disulfide bridge reduction; development; NTR;
KW hair care product; venom neutralisation; food technology; food allergy;
KW NADPH-redoxin reductase; ss.
XX
OS Hordeum vulgare.
XX
PN WO200058352-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US08566.
XX
PR 31-MAR-1999; 99US-0127198.
PR 06-DEC-1999; 99US-0169162.
PR 21-JAN-2000; 2000US-0177739.
PR 21-JAN-2000; 2000US-0177740.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Cho M, Del Val G, Caillau M, Lemaux PG, Buchanan BB;
XX
DR WPI; 2000-679291/66.
XX
PT Recombinant or isolated nucleic acid, useful for producing transgenic
PT plants with altered redox properties, encode thioredoxin h or
PT thioredoxin reductase -
XX
PS Disclosure; Fig 12; 125pp; English.
XX
CC The present invention relates to the isolation and use of the barley
CC thioredoxin h and NADPH-redoxin reductase coding and protein sequences.
CC Thioredoxin is thought to be involved in plant development via its
CC function in the reduction of disulfide bridges. Thioredoxin can be used
CC in hair care products and in the neutralisation of some venoms and
CC toxins, and is also useful in the reduction of some food, for example it
CC can be used to reduce the allergenicity of foods and the digestibility
CC of some proteins. It can also be used to enhance the baking qualities of
CC cereal flour.
XX
SQ Sequence 497 BP; 138 A; 150 C; 89 G; 120 T; 0 other;

alignment_scores:
Quality: 86.00 Length: 20
Ratio: 4.300 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-538-864-4 x AAC62462 ..

```
Align seg 1/1  to: AAC62462  from: 1  to: 497

       1 AlaLysArgLeuValLeuPheValAlaValIleValAlaLeuValAlaLe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     438 GCTAAGCGGCTGGTCCTCTTTGTGGCGGTAATCGTCGCCCTCGTGGCTCT 487

      17 uThrThrAla 20
         ||||||||||
     488 CACCACCGCT 497

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:AAV20662

seq_documentation_block:
ID   AAV20662 standard; DNA; 2296 BP.
XX
AC   AAV20662;
XX
DT   23-JUN-1998  (first entry)
XX
DE   Barley D-hordein gene 5'-terminal region.
XX
KW   Barley; D-hordein; DPP3; promoter; gene expression; regulation;
KW   seed; structural gene; ds.
XX
OS   Hordeum vulgare.
XX
PN   WO9803655-A2.
XX
PD   29-JAN-1998.
XX
PF   22-JUL-1997;   97WO-JP02526.
XX
PR   23-JUL-1996;   96JP-0193433.
XX
PA   (SAPB ) SAPPORO BREWERIES.
XX
PI   Hirota N,  Ito K,  Kihara M,  Kuroda H;
XX
DR   WPI; 1998-120779/11.
XX
PT   Gene expression regulatory DNA, expression cassettes and vectors -
PT   comprising promoter region from barley, Hordeum vulgare, D-hordein
PT   gene, useful to control expression of desired gene e.g. to improve
PT   seeds
XX
PS   Example 3; Page 25-26; 42pp; English.
XX
CC   The present sequence represents the 5'-terminal region of the barley
CC   D-hordein gene. The present invention describes gene expression
CC   regulatory DNA which comprises a promoter region derived from the
CC   barley (Hordeum vulgare) D-hordein gene which allows expression of a
CC   desired structural gene, and a regulatory region regulating such
CC   expression. The introduction into plants of expression cassettes
CC   containing the gene expression regulatory DNA (either directly or via
CC   expression vectors) enables the expression of a gene within a plant cell
CC   e.g. barley to be controlled. The use of activating and suppressing
CC   regions in the regulatory DNA allows control of expression by e.g.
```

CC tissue type or developmental stage, whilst the use of only an activating
CC region maintains expression at a high level, providing an effective
CC production means when recovery of the product of the structural gene is
CC desired. The expression cassette/vector may be introduced into e.g.
CC maturing seed endosperm tissue or regeneratable plant cells (e.g. derived
CC from anthers) to improve seeds of barley or other plants, to produce
CC gene products in seeds or to contribute to plant breeding programmes.
CC The expression regulatory DNA can also used in expression systems in
CC vitro. GUS activity in barley protoplasts transfected with plasmid
CC DPP3GUS2 comprising isolated D-hordein promoter region was 1.5 times
CC higher than in those transfected with control pACT1F.
XX
SQ Sequence 2296 BP; 629 A; 708 C; 606 G; 353 T; 0 other;

alignment_scores:
Quality: 86.00 Length: 20
Ratio: 4.300 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-538-864-4 x AAV20662 ..

Align seg 1/1 to: AAV20662 from: 1 to: 2296

```
      1 AlaLysArgLeuValLeuPheValAlaValIleValAlaLeuValAlaLe 17
        |||||||||||||||||||||||||||||||||||||||||||||||||||
     40 GCTAAGCGGCTGGTCCTCTTTGTGGCGGTAATCGTCGCCCTCGTGGCTCT 89

     17 uThrThrAla 20
        ||||||||||
     90 CACCACCGCT 99
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF63380

seq_documentation_block:
ID AAF63380 standard; cDNA; 2380 BP.
XX
AC AAF63380;
XX
DT 10-MAY-2001 (first entry)
XX
DE Barley cDNA involved in D-hordein production SEQ ID 2.
XX
KW Barley; gel protein; D-hordein; malt; wort filterability; extraction; ss.
XX
OS Hordeum vulgare.
XX
PN WO200111946-A1.
XX
PD 22-FEB-2001.
XX
PF 16-AUG-2000; 2000WO-JP05476.
XX
PR 16-AUG-1999; 99JP-0229696.
XX
PA (SAPB) SAPPORO BREWERIES LTD.

XX
PI Hirota N, Kihara M, Ito K;
XX
DR WPI; 2001-191587/19.
XX
PT Transformation of barley with a D-hordein expression regulator for
PT production of barley with lowered gel protein content -
XX
PS Claim 4; Page 33-34; 40pp; Japanese.
XX
CC This invention relates to barley having a low gel protein content. The
CC barley is transformed with a polynucleotide sequence which regulated the
CC formation of D-hordein. Transformation results in the production of
CC barley strains with improved malting properties such as wort
CC filterability and efficiency of extraction. The present sequence
CC represents cDNA involved in the regulation of D-hordein production.
XX
SQ Sequence 2380 BP; 642 A; 747 C; 622 G; 369 T; 0 other;

alignment_scores:
            Quality: 86.00   Length: 20
              Ratio: 4.300   Gaps: 0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-538-864-4 x AAF63380   ..

 Align seg 1/1 to: AAF63380 from: 1 to: 2380

       1 AlaLysArgLeuValLeuPheValAlaValIleValAlaLeuValAlaLe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      27 GCTAAGCGGCTGGTCCTCTTTGTGGCGGTAATCGTCGCCCTCGTGGCTCT 76

      17 uThrThrAla 20
         ||||||||||
      77 CACCACCGCT 86

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF63379

seq_documentation_block:
ID AAF63379 standard; cDNA; 2434 BP.
XX
AC AAF63379;
XX
DT 10-MAY-2001 (first entry)
XX
DE Barley cDNA involved in D-hordein production SEQ ID 1.
XX
KW Barley; gel protein; D-hordein; malt; wort filterability; extraction; ss.
XX
OS Hordeum vulgare.
XX
PN WO200111946-A1.
XX
PD 22-FEB-2001.
XX

PF 16-AUG-2000; 2000WO-JP05476.
XX
PR 16-AUG-1999; 99JP-0229696.
XX
PA (SAPB) SAPPORO BREWERIES LTD.
XX
PI Hirota N, Kihara M, Ito K;
XX
DR WPI; 2001-191587/19.
XX
PT Transformation of barley with a D-hordein expression regulator for
PT production of barley with lowered gel protein content -
XX
PS Claim 4; Page 31-33; 40pp; Japanese.
XX
CC This invention relates to barley having a low gel protein content. The
CC barley is transformed with a polynucleotide sequence which regulated the
CC formation of D-hordein. Transformation results in the production of
CC barley strains with improved malting properties such as wort
CC filterability and efficiency of extraction. The present sequence
CC represents cDNA involved in the regulation of D-hordein production.
XX
SQ Sequence 2434 BP; 675 A; 757 C; 626 G; 376 T; 0 other;

alignment_scores:
            Quality: 86.00   Length: 20
              Ratio: 4.300   Gaps: 0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-538-864-4 x AAF63379   ..

 Align seg 1/1 to: AAF63379 from: 1 to: 2434

       1 AlaLysArgLeuValLeuPheValAlaValIleValAlaLeuValAlaLe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      40 GCTAAGCGGCTGGTCCTCTTTGTGGCGGTAATCGTCGCCCTCGTGGCTCT 89

      17 uThrThrAla 20
         ||||||||||
      90 CACCACCGCT 99

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:AAI70852

seq_documentation_block:
ID AAI70852 standard; DNA; 1302 BP.
XX
AC AAI70852;
XX
DT 18-FEB-2002 (first entry)
XX
DE Wheat glutenin gene variant.
XX
KW Wheat; glutenin; storage protein; variant; transgenic plant;
KW gluten; ds.
XX

OS Triticum aestivum.
XX
FH Key Location/Qualifiers
FT allele replace(1181,C)
FT /*tag= a
XX
PN WO200179477-A2.
XX
PD 25-OCT-2001.
XX
PF 13-APR-2001; 2001WO-HU00045.
XX
PR 14-APR-2000; 2000HU-0001563.
XX
PA (MAGY) MTA MEZOGAZDASAGI KI.
XX
PI Juhasz A, Tamas L, Bedo Z, Vida G, Karsai I, Lang L;
PI Tamasne Nyitrai E;
XX
DR WPI; 2002-017612/02.
DR P-PSDB; AAM50386.
XX
PT A new nucleic acid comprising a variant allele of the lAx2asteriskHMW
PT glutenin subunit gene of wheat has at least one extra cysteine codon
PT and is useful for developing new wheat varieties with enhanced quality
PT gluten -
XX
PS Disclosure; Fig 4b; 28pp; English.
XX
CC The present sequence is that of the coding region of a newly
CC identified allele, designated 1Ax2asteriskB, of the 1Ax2asterisk
CC HMW glutenin subunit gene, found in certain lines of wheat
CC variety Bankuti 1201. The variant differs from the 1Ax2asterisk
CC gene by a single point mutation of C to G at nucleotide position
CC 1181. This results in a change from Ser to Cys at amino acid
CC position 394. Because of this, the newly identified allele
CC provides enhanced possibilities for the formation of disulfide
CC bridges compared with the known allele, and this could at least
CC partly explain the good technological properties of the variety.
CC The newly identified gene can be used to develop transgenic
CC wheat varieties with better quality gluten.
XX
SQ Sequence 1302 BP; 439 A; 364 C; 327 G; 172 T; 0 other;

alignment_scores:
Quality: 72.00 Length: 19
Ratio: 3.789 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 84.211

alignment_block:
US-09-538-864-4 x AAI70852 ..

Align seg 1/1 to: AAI70852 from: 1 to: 1302

2 LysArgLeuValLeuPheValAlaValIleValAlaLeuValAlaLeuTh 18
||||||||||||||||||:::||||||:::||||||||||||||||||

```
 7 AAGCGGTTGGTTCTTTTTGCGGCGGTAGTCGTCGCCCTTGTGGCTCTCAC 56

18 rThrAla 20
   |:::|||
57 CGCTGCT 63
```

```
seq_documentation_block:
; Sequence 2, Application US/08899336
; Patent No. 5955649
;  GENERAL INFORMATION:
;    APPLICANT:  HIROTA, NAOHIKO
;    APPLICANT:  KIHARA, MAKOTO
;    APPLICANT:  KURODA, HISAO
;    APPLICANT:  ITO, KAZUTOSHI
;    TITLE OF INVENTION:  GENE EXPRESSION REGULATORY DNA,
;    TITLE OF INVENTION:  EXPRESSION CASSETTE, EXPRESSION VECTOR AND TRANSGENIC
;    TITLE OF INVENTION:  PLANT
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/899,336
;      FILING DATE:  23-JUL-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP HEI 8-193433
;      FILING DATE:  23-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  2589-0061-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2296 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-899-336-2


alignment_scores:
            Quality:   86.00              Length:     20
              Ratio:  4.300                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-538-864-4 x US-08-899-336-2    ..
```

Checked
Ø

Align seg 1/1 to: US-08-899-336-2 from: 1 to: 2296

```
      1 AlaLysArgLeuValLeuPheValAlaValIleValAlaLeuValAlaLe 17
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     40 GCTAAGCGGCTGGTCCTCTTTGTGGCGGTAATCGTCGCCCTCGTGGCTCT 89

     17 uThrThrAla 20
        |||||||||
     90 CACCACCGCT 99
```

```
seq_documentation_block:
ID   AAX34624 standard; DNA; 486 BP.
XX
AC   AAX34624;
XX
DT   01-JUL-1999  (first entry)
XX
DE   Barley B1 hordein promoter and signal sequence.
XX
KW   Seed maturation-specific promoter; seed; transgenic plant; rice; barley;
KW   maize; wheat; oat; rye; sorghum; millet; tricalate plant; insulin;
KW   interferon; erythropoietin; interleukin; nutritional supplement;
KW   grain quality; B1 hordein promoter; signal sequence; ss.
XX
OS   Hordeum vulgare.
XX
FH   Key             Location/Qualifiers
FT   CDS             430..486
FT                   /*tag=  a
FT                   /note= "fragment encoding barley B1 hordein
FT                          signal peptide"
XX
PN   WO9916890-A2.
XX
PD   08-APR-1999.
XX
PF   30-SEP-1998;   98WO-US20691.
XX
PR   30-SEP-1997;   97US-0060510.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Buchanan RB,  Cho M,  Lemaux PG;
XX
DR   WPI; 1999-255099/21.
DR   P-PSDB; AAY06897.
XX
PT   New recombinant nucleic acid molecules
XX
PS   Examples; Fig 3; 48pp; English.
XX
CC   The invention relates to recombinant nucleic acid molecules which contain
CC   a seed maturation-specific promoter for expression of a selected
CC   polypeptide in seeds of transgenic plants. The novel recombinant nucleic
CC   acid molecule (NAM) has a structure P-X or P-SS-X, where X is a NAM
CC   encoding a polypeptide, P is a seed maturation-specific promoter, and SS
CC   is a signal sequence that targets a linked polypeptide to an
CC   intracellular body. The recombinant NAMs can be used for producing
CC   transgenic plants such as rice, barley, maize, wheat, oat, rye, sorghum,
CC   millet or tricalate plants.  The transgenic plants can be used for
CC   producing a selected polypeptide in seeds of the plants.  They can be
CC   used to produce polypeptides such as insulin, interferons, erythropoietin
CC   and interleukins, or nutritional supplements. Alternatively the
CC   polypeptide can improve the quality of grain. The present sequence
CC   represents the nucleic acid sequence of a barley B1 hordein promoter and
CC   signal sequence.
XX
```

```
SQ   Sequence 486 BP; 176 A; 107 C; 79 G; 124 T; 0 other;


alignment_scores:
            Quality:   85.00              Length:     19
              Ratio:  4.474                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-538-864-2 x AAX34624   ..

 Align seg 1/1  to: AAX34624  from: 1  to: 486

       1 MetLysThrPheLeuIlePheAlaLeuLeuAlaIleAlaAlaThrSerTh 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     430 ATGAAGACCTTCCTCATCTTTGCACTCCTCGCCATTGCGGCAACAAGTAC 479

      17 rIleAla 19
         |||||||
     480 GATTGCA 486

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAC61535

seq_documentation_block:
ID   AAC61535 standard; DNA; 486 BP.
XX
AC   AAC61535;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Nucleotide sequence of the D-hordein promoter and signal sequence.
XX
KW   Transgenic plant; thioredoxin; edible seed; food; feed; beverage;
KW   allergenicity; germination rate; flour; malabsorption syndrome;
KW   coeliac disease; sprue; catarrhal dysentery; brewing; malting;
KW   industrial alcohol; food additive; D-hordein promoter; ss.
XX
OS   Hordeum vulgare.
XX
FH   Key             Location/Qualifiers
FT   promoter        1..429
FT                   /*tag=  a
FT   sig_peptide     430..486
FT                   /*tag=  b
XX
PN   WO200058453-A2.
XX
PD   05-OCT-2000.
XX
PF   29-MAR-2000; 2000WO-US08315.
XX
PR   29-MAR-1999;   99US-0126736.
PR   31-MAR-1999;   99US-0127198.
PR   06-DEC-1999;   99US-0169162.
PR   21-JAN-2000; 2000US-0177739.
PR   21-JAN-2000; 2000US-0177740.
XX
```

PA (REGC) UNIV CALIFORNIA.
XX
PI Cho M, Lemaux PG, Buchanan BB, Wong J, Marx C;
XX
DR WPI; 2000-611708/58.
XX
PT Transgenic plants overexpressing thioredoxin protein, and their
PT applications to enhance baking quality, digestibility, brewing and
PT malting operations, and reduce allergenicity -
XX
PS Example 1; Fig 6; 103pp; English.
XX
CC The specification describes transgenic plants in which have an increased
CC specific activity of thioredoxin compared to a non-transgenic plant of
CC the same species. The transgenic plants provide edible seeds or grains
CC for processing and consumption as food, feed, or beverage products by
CC humans and other animals which have reduced allergenicity, increased
CC digestibility, and improved germination rate. For humans, particular
CC food products improved which can be improved include flour, as bread,
CC pasta, cookies, and cake. The dough has increased strength and volume,
CC improving baking qualities. Improved enzyme contents (pullulanase and
CC amylase) improve digestibility of endogenous starches and proteins,
CC reducing malabsorption syndromes in certain subjects (e.g., coeliac
CC disease, sprue, and catarrhal dysentery patients), and allowing wider
CC consumption. Fermentability, of application in the brewing and malting
CC industries, and for production of industrial alcohol and malt as such,
CC is also improved. Products from transgenic plants may also be used as
CC food additives. The present sequence represents the barley
CC endosperm-specific D-hordein promoter and the signal sequence. It is
CC used in the course of the invention, to produce transgenic plants.
XX
SQ Sequence 486 BP; 176 A; 107 C; 79 G; 124 T; 0 other;

alignment_scores:
Quality: 85.00 Length: 19
Ratio: 4.474 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-538-864-2 x AAC61535 ..

Align seg 1/1 to: AAC61535 from: 1 to: 486

```
      1 MetLysThrPheLeuIlePheAlaLeuLeuAlaIleAlaAlaThrSerTh 17
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    430 ATGAAGACCTTCCTCATCTTTGCACTCCTCGCCATTGCGGCAACAAGTAC 479

     17 rIleAla 19
        |||||||
    480 GATTGCA 486
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAC62461

seq_documentation_block:
ID AAC62461 standard; cDNA; 486 BP.
XX

AC AAC62461;
XX
DT 07-FEB-2001 (first entry)
XX
DE Barley B1-hordein promoter and signal sequence.
XX
KW Barley; thioredoxin h; disulfide bridge reduction; development; NTR;
KW hair care product; venom neutralisation; food technology; food allergy;
KW NADPH-redoxin reductase; ss.
XX
OS Hordeum vulgare.
XX
PN WO200058352-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US08566.
XX
PR 31-MAR-1999; 99US-0127198.
PR 06-DEC-1999; 99US-0169162.
PR 21-JAN-2000; 2000US-0177739.
PR 21-JAN-2000; 2000US-0177740.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Cho M, Del Val G, Caillau M, Lemaux PG, Buchanan BB;
XX
DR WPI; 2000-679291/66.
XX
PT Recombinant or isolated nucleic acid, useful for producing transgenic
PT plants with altered redox properties, encode thioredoxin h or
PT thioredoxin reductase -
XX
PS Example 3; Fig 11; 125pp; English.
XX
CC The present invention relates to the isolation and use of the barley
CC thioredoxin h and NADPH-redoxin reductase coding and protein sequences.
CC Thioredoxin is thought to be involved in plant development via its
CC function in the reduction of disulfide bridges. Thioredoxin can be used
CC in hair care products and in the neutralisation of some venoms and
CC toxins, and is also useful in the reduction of some food, for example it
CC can be used to reduce the allergenicity of foods and the digestibility
CC of some proteins. It can also be used to enhance the baking qualities of
CC cereal flour.
XX
SQ Sequence 486 BP; 176 A; 107 C; 79 G; 124 T; 0 other;

alignment_scores:
            Quality: 85.00   Length: 19
              Ratio: 4.474   Gaps: 0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-538-864-2 x AAC62461   ..

 Align seg 1/1 to: AAC62461 from: 1 to: 486

```
  1 MetLysThrPheLeuIlePheAlaLeuLeuAlaIleAlaAlaThrSerTh 17
    ||||||||||||||||||||||||||||||||||||||||||||||||||
430 ATGAAGACCTTCCTCATCTTTGCACTCCTCGCCATTGCGGCAACAAGTAC 479

 17 rIleAla 19
    |||||||
480 GATTGCA 486
```

100% SID 2

```
seq_documentation_block:
LOCUS       HVB1HOR2                1775 bp    DNA     linear   PLN 22-MAY-1995
DEFINITION  H.vulgare B1 hordein gene.
ACCESSION   X87232
VERSION     X87232.1  GI:809030
KEYWORDS    B1 hordein; Hor2-4 gene.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 1775)
  AUTHORS   Brandt,A., Montembault,A., Cameron Mills,V. and Rasmussen,S.
  TITLE     Primary structure of a B1 hordein gene from barley
  JOURNAL   Carlsberg Res. Commun. 50, 333-345 (1985)
FEATURES             Location/Qualifiers
     source          1. .1775
                     /organism="Hordeum vulgare"
                     /cultivar="Carlsberg II"
                     /db_xref="taxon:4513"
                     /chromosome="5"
                     /clone="hor2-4"
                     /clone_lib="lambda L47.1"
                     /dev_stage="immature endosperm"
     repeat_region   join(115. .124,248. .257)
                     /rpt_unit=115. .124
     CAAT_signal     422. .425
     TATA_signal     472. .475
     gene            551. .1366
                     /gene="hor2-4"
     CDS             551. .1366
                     /gene="hor2-4"
                     /codon_start=1
                     /product="B1 hordein"
                     /protein_id="CAA60681.1"
                     /db_xref="GI:809031"
                     /db_xref="SPTREMBL:Q40021"
                     /translation="MKTFLIFALLAIAATSTIAQQQPFPQQPIPQQPQPYPQQPQPYP
                     QQPFPPQQAFPQQPPFWPQQPFPQQPPFGLQQPILSQQQPCTPQPTPLPQGQLYQTLL
                     QLQIPYVQPSILQQLTPCKVFLQQQCSPVRMPQLIARSQMLQQSSCHVLQQQCCQQLP
                     QIPEQFRHEAIRAIVYSIFLQEQPQQSVQGASQPQQQLQEEQVGQCYFQQPQPQQLGQ
                     PQQVPQSVFLQPHQIAQLEATNSIALRTLPTMCNVNVPLYDIMPFGVGTRVGV"
     mat_peptide     605. .1363
                     /gene="hor2-4"
                     /product="B1 hordein"
     polyA_signal    1433. .1438
     polyA_signal    1491. .1496
     polyA_signal    1501. .1506
BASE COUNT      573 a    473 c    305 g    424 t
ORIGIN


alignment_scores:
            Quality:   85.00              Length:     19
              Ratio:  4.474                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
```

```
alignment_block:
 US-09-538-864-2 x HVB1HOR2    ..

 Align seg 1/1  to: HVB1HOR2  from: 1  to: 1775

       1 MetLysThrPheLeuIlePheAlaLeuLeuAlaIleAlaAlaThrSerTh 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     551 ATGAAGACCTTCCTCATCTTTGCACTCCTCGCCATTGCGGCAACAAGTAC 600

      17 rIleAla 19
         |||||||
     601 GATTGCA 607

seq_name: gb_pl:HVB1HORG

seq_documentation_block:
LOCUS       HVB1HORG               2900 bp    DNA     linear   PLN 21-MAR-1995
DEFINITION  Barley gene for B1 hordein.
ACCESSION   X03103
VERSION     X03103.1  GI:18909
KEYWORDS    direct repeat; hordein; prolamin; seed storage protein; signal
            peptide; storage protein.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 2900)
  AUTHORS   Forde,B.G., Heyworth,A., Pywell,J. and Kreis,M.
  TITLE     Nucleotide sequence of a B1 hordein gene and the identification of
            possible upstream regulatory elements in endosperm storage protein
            genes from barley, wheat and maize
  JOURNAL   Nucleic Acids Res. 13 (20), 7327-7339 (1985)
  MEDLINE   86041918
FEATURES             Location/Qualifiers
     source          1. .2900
                     /organism="Hordeum vulgare"
                     /db_xref="taxon:4513"
     repeat_region   1. .18
                     /note="imp. direct repeat"
     misc_feature    1. .22
                     /note="put. regulatory region"
     misc_feature    262. .295
                     /note="put. regulatory region"
     repeat_region   275. .292
                     /note="imp. direct repeat"
     misc_feature    426. .435
                     /note="put. regulatory region, CATC-box"
     promoter        485. .492
                     /note="put. TATA-box"
     precursor_RNA   513. .1579
                     /note="put. primary transcript"
     CDS             564. .1445
                     /note="precursor"
                     /codon_start=1
                     /protein_id="CAA26889.1"
                     /db_xref="GI:18910"
```

```
                     /db_xref="SWISS-PROT:P06470"
                     /translation="MKTFLIFALLAIAATSTIAQQQPFPQQPIPQQPQPYPQQPQPYP
                     QQPFPPQQPFPQQPVPQQPQPYPQQPFPPQQPFPQQPPFWQQKPFPQQPPFGLQQPIL
                     SQQQPCTPQQTPLPQGQLYQTLLQLQIQYVHPSILQQLNPCKVFLQQQCSPVPVPQRI
                     ARSQMLQQSSCHVLQQQCCQQLPQIPEQFRHEAIRAIVYSIFLQEQPQQLVEGVSQPQ
                     QQLWPQQVGQCSFQQPQPQQVGQQQQVPQSAFLQPHQIAQLEATTSIALRTLPMMCSV
                     NVPLYRILRGVGPSVGV"
     sig_peptide     564. .620
                     /note="putative"
     mat_peptide     621. .1442
                     /product="mature B1 hordein (aa 1-274)"
     misc_feature    1499. .1504
                     /note="pot. polyadenylation signal"
     misc_feature    1556. .1561
                     /note="pot. polyadenylation signal"
     misc_feature    1567. .1572
                     /note="pot. polyadenylation signal"
     polyA_site      1579
                     /note="put. polyadenylation site"
BASE COUNT      938 a    763 c    495 g    704 t
ORIGIN


alignment_scores:
            Quality:   85.00              Length:     19
              Ratio:  4.474                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-538-864-2 x HVB1HORG   ..

 Align seg 1/1  to: HVB1HORG  from: 1  to: 2900

       1 MetLysThrPheLeuIlePheAlaLeuLeuAlaIleAlaAlaThrSerTh 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     564 ATGAAGACCTTCCTCATCTTTGCACTCCTCGCCATTGCGGCAACAAGTAC 613

      17 rIleAla 19
         |||||||
     614 GATTGCG 620

seq_name: gb_pl:HVBHO47
```